

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/047,608
Source: 1Fw16
Date Processed by STIC: 8/20/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/20/2005

PATENT APPLICATION: US/10/047,608

TIME: 11:21:10

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\08202005\J047608.raw

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3 <110> APPLICANT: Bell, Leonard
5 <120> TITLE OF INVENTION: METHOD OF PROPHYLAXIS AGAINST LARGE MYOCARDIAL INFARCTIONS
7 <130> FILE REFERENCE: 59
9 <140> CURRENT APPLICATION NUMBER: 10/047,608
10 <141> CURRENT FILING DATE: 2002-01-14
12 <150> PRIOR APPLICATION NUMBER: US 60/262,540
13 <151> PRIOR FILING DATE: 2001-01-18
15 <160> NUMBER OF SEQ ID NOS: 18
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 747
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Humanized antibody
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(744)
32 <400> SEQUENCE: 1
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34 Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
35 1          5          10          15
37 gtg ggc gat agg gtc acc atc acc tgc ggc gcc agc gaa aac atc tat      96
38 Val Gly Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
39          20          25          30
41 ggc gcg ctg aac tgg tat caa cgt aaa cct ggg aaa gct ccg aag ctt      144
42 Gly Ala Leu Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu
43          35          40          45
45 ctg att tac ggt gcg acg aac ctg gca gat gga gtc cct tct cgc ttc      192
46 Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe
47          50          55          60
49 tct gga tcc ggc tcc gga acg gat ttc act ctg acc atc agc agt ctg      240
50 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
51 65          70          75          80
53 cag cct gaa gac ttc gct acg tat tac tgt cag aac gtt tta aat act      288
54 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr
55          85          90          95
57 ccg ttg act ttc gga cag ggt acc aag gtg gaa ata aaa cgt act ggc      336
58 Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly
59          100          105          110
61 ggt ggt ggt tct ggt ggc ggt gga tct ggt ggt ggc ggt tct caa gtc      384
62 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
63          115          120          125

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65  caa  ctg  gtg  caa  tcc  ggc  gcc  gag  gtc  aag  aag  cca  ggg  gcc  tca  gtc      432
66  Gln  Leu  Val  Gln  Ser  Gly  Ala  Glu  Val  Lys  Lys  Pro  Gly  Ala  Ser  Val
67      130                      135                      140
69  aaa  gtg  tcc  tgt  aaa  gct  agc  ggc  tat  att  ttt  tct  aat  tat  tgg  att      480
70  Lys  Val  Ser  Cys  Lys  Ala  Ser  Gly  Tyr  Ile  Phe  Ser  Asn  Tyr  Trp  Ile
71  145                      150                      155                      160
73  caa  tgg  gtg  cgt  cag  gcc  ccc  ggg  cag  ggc  ctg  gaa  tgg  atg  ggt  gag      528
74  Gln  Trp  Val  Arg  Gln  Ala  Pro  Gly  Gln  Gly  Leu  Glu  Trp  Met  Gly  Glu
75      165                      170                      175
77  atc  tta  ccg  ggc  tct  ggt  agc  acc  gaa  tat  acc  gaa  aat  ttt  aaa  gac      576
78  Ile  Leu  Pro  Gly  Ser  Gly  Ser  Thr  Glu  Tyr  Thr  Glu  Asn  Phe  Lys  Asp
79      180                      185                      190
81  cgt  gtt  act  atg  acg  cgt  gac  act  tcg  act  agt  aca  gta  tac  atg  gag      624
82  Arg  Val  Thr  Met  Thr  Arg  Asp  Thr  Ser  Thr  Ser  Thr  Val  Tyr  Met  Glu
83      195                      200                      205
85  ctc  tcc  agc  ctg  cga  tcg  gag  gac  acg  gcc  gtc  tat  tat  tgc  gcg  cgt      672
86  Leu  Ser  Ser  Leu  Arg  Ser  Glu  Asp  Thr  Ala  Val  Tyr  Tyr  Cys  Ala  Arg
87      210                      215                      220
89  tat  ttt  ttt  ggt  tct  agc  ccg  aat  tgg  tat  ttt  gat  gtt  tgg  ggt  caa      720
90  Tyr  Phe  Phe  Gly  Ser  Ser  Pro  Asn  Trp  Tyr  Phe  Asp  Val  Trp  Gly  Gln
91  225                      230                      235                      240
93  gga  acc  ctg  gtc  act  gtc  tcg  agc  tga      747
94  Gly  Thr  Leu  Val  Thr  Val  Ser  Ser
95      245
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 248
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Synthetic Construct
106 <400> SEQUENCE: 2
108 Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
109 1      5      10      15
112 Val Gly Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
113      20      25      30
116 Gly Ala Leu Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu
117      35      40      45
120 Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe
121      50      55      60
124 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
125 65      70      75      80
128 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr
129      85      90      95
132 Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly
133      100     105     110
136 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
137      115     120     125
140 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
141      130     135     140

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144 Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
145 145 150 155 160
148 Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu
149 165 170 175
152 Ile Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe Lys Asp
153 180 185 190
156 Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
157 195 200 205
160 Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
161 210 215 220
164 Tyr Phe Phe Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
165 225 230 235 240
168 Gly Thr Leu Val Thr Val Ser Ser
169 245
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 747
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Humanized antibody
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (1)..(744)
185 <400> SEQUENCE: 3
186 atg gcc gat atc cag atg acc cag tcc ccg tcc tcc ctg tcc gcc tct 48
187 Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
188 1 5 10 15
190 gtg ggc gat agg gtc acc atc acc tgc ggc gcc agc gaa aac atc tat 96
191 Val Gly Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
192 20 25 30
194 ggc gcg.ctg aac tgg tat caa cag aaa cct ggg aaa gct ccg aag ctt 144
195 Gly Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
196 35 40 45
198 ctg att tac ggt gcg acg aac ctg gca gat gga gtc cct tct cgc ttc 192
199 Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe
200 50 55 60
202 tct gga tcc ggc tcc gga acg gat ttc act ctg acc atc agc agt ctg 240
203 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
204 65 70 75 80
206 cag cct gaa gac ttc gct acg tat tac tgt cag aac gtt tta aat act 288
207 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr
208 85 90 95
210 ccg ttg act ttc gga cag ggt acc aag gtg gaa ata aaa cgt act ggc 336
211 Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly
212 100 105 110
214 ggt ggt ggt tct ggt ggc ggt gga tct ggt ggt ggc ggt tct caa gtc 384
215 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
216 115 120 125
218 caa ctg gtg caa tcc ggc gcc gag gtc aag aag cca ggg gcc tca gtc 432

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219 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
220      130      135      140
222 aaa gtg tcc tgt aaa gct agc ggc tat att ttt tct aat tat tgg att      480
223 Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
224 145      150      155      160
226 caa tgg gtg cgt cag gcc ccc ggg cag ggc ctg gaa tgg atg ggt gag      528
227 Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu
228      165      170      175
230 atc tta ccg ggc tct ggt agc acc gaa tat gcc caa aaa ttc cag ggc      576
231 Ile Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe Gln Gly
232      180      185      190
234 cgt gtt act atg acg cgt gac act tcg act agt aca gta tac atg gag      624
235 Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
236      195      200      205
238 ctc tcc agc ctg cga tcg gag gac acg gcc gtc tat tat tgc gcg cgt      672
239 Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
240      210      215      220
242 tat ttt ttt ggt tct agc ccg aat tgg tat ttt gat gtt tgg ggt caa      720
243 Tyr Phe Phe Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
244 225      230      235      240
246 gga acc ctg gtc act gtc tcg agc tga      747
247 Gly Thr Leu Val Thr Val Ser Ser
248      245
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 248
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Synthetic Construct
259 <400> SEQUENCE: 4
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262 1      5      10      15
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266      20      25      30
269 Gly Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
270      35      40      45
273 Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe
274      50      55      60
277 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
278 65      70      75      80
281 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr
282      85      90      95
285 Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly
286      100      105      110
289 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
290      115      120      125
293 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
294      130      135      140
297 Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile

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298 145          150          155          160
301 Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu
302          165          170          175
305 Ile Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe Gln Gly
306          180          185          190
309 Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
310          195          200          205
313 Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
314          210          215          220
317 Tyr Phe Phe Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
318 225          230          235          240
321 Gly Thr Leu Val Thr Val Ser Ser
322          245
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 747
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Humanized antibody
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (1)..(744)
338 <400> SEQUENCE: 5
339 atg gcc gat atc cag atg acc cag tcc ccg tcc tcc ctg tcc gcc tct      48
340 Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
341 1          5          10          15
343 gtg ggc gat agg gtc acc atc acc tgc ggc gcc agc gaa aac atc tat      96
344 Val Gly Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
345          20          25          30
347 ggc gcg ctg aac tgg tat caa cag aaa ccc ggg aaa gct ccg aag ctt      144
348 Gly Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
349          35          40          45
351 ctg att tac ggt gcg acg aac ctg gca gat gga gtc cct tct cgc ttc      192
352 Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe
353          50          55          60
355 tct gga tcc ggc tcc gga acg gat ttc act ctg acc atc agc agt ctg      240
356 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
357 65          70          75          80
359 cag cct gaa gac ttc gct acg tat tac tgt cag aac gtt tta aat act      288
360 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr
361          85          90          95
363 ccg ttg act ttc gga cag ggt acc aag gtg gaa ata aaa cgt act ggc      336
364 Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly
365          100          105          110
367 ggt ggt ggt tct ggt ggc ggt gga tct ggt ggt ggc ggt tct caa gtc      384
368 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
369          115          120          125
371 caa ctg gtg caa tcc ggc gcc gag gtc aag aag cca ggg gcc tca gtc      432
372 Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/20/2005
PATENT APPLICATION: US/10/047,608 TIME: 11:21:11

Input Set : A:\Sequence Listing.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY

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